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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/713,208	11/17/2003	Jian Ni	PF381C1D1	5854

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EXAMINER	
HUYNH, PHUONG N	

ART UNIT	PAPER NUMBER
1644	

DATE MAILED: 03/22/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

4

Office Action Summary	Application No.	Applicant(s)	
	10/713,208	NI ET AL.	
	Examiner	Art Unit	
	Phuong Huynh	1644	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE *Three* MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *02 December 2004*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *9,11 and 13-23* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *9, 11 and 13-23* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

4/6

DETAILED ACTION

1. Claims 9, 11 and 13-23 are pending.

2. In view of the amendment filed 12/20/04, the following rejections remain.

3. The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

4. Claims 9, 18, 20, 22 and 23 stand rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

It is apparent that cDNA in ATCC with the Deposit No. 209038 as set forth in claims 9 and 18 is required to practice the claimed invention. As a required element, it must be known and readily available to the public or obtainable by a repeatable method set forth in the specification. If it is not so obtainable or available, the enablement requirements of 35 USC 112, a deposit of the clone may satisfy first paragraph. See 37 CFR 1.801-1.809.

If the deposit has been made under the terms of the Budapest Treaty, an affidavit or declaration by applicants or someone associated with the patent owner who is in a position to make such assurances, or a statement by an attorney of record over his or her signature, stating that the cDNA in ATCC with the Deposit No. 209038 has been deposited under the Budapest Treaty and that the cDNA in ATCC with the Deposit No. 209038 will be irrevocably and without restriction or condition released to the public upon the issuance of a patent would satisfy the deposit requirement made herein. See 37 CFR 1.808. Further, the record must be clear that the deposit will be maintained in a public depository for a period of 30 years after the date of deposit or 5 years after the last request for a sample or **for the enforceable life of the patent whichever is longer**. See 37 CFR 1.806.

If the deposit has not been made under the Budapest Treaty, then an affidavit or declaration by applicants or someone associated with the patent owner who is in a position to make such assurances, or a statement by an attorney of record over his or her signature must be

made, stating that the deposit has been made at an acceptable depository and that the criteria set forth in 37 CFR 1.801-1.809, have been met.

As an additional means for completing the record, applicant may submit a copy of the contract with the depository for deposit and maintenance of each deposit throughout the life of the patent.

Applicants' arguments filed 12/20/04 have been fully considered but are not found persuasive.

Applicants' position is that a partially redacted copy of the ATCC Deposit Receipt for Accession Number 209038 is enclosed as Exhibit A.

However, Exhibit A is not found in amendment filed 12/20/04.

5. Claims 9, 13-17, and 19-23 stand rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for (1) an isolated I-FLICE-2 polypeptide comprising an amino acid sequence selected from the group consisting of: amino acids from 1 to 348 in SEQ ID NO: 6, amino acids from 2 to 348 in SEQ ID NO: 6, (2) the said polypeptide wherein the polypeptide is glycosylated for a method of inhibiting apoptosis mediated by TNFR-1 and CD95, **does not** reasonably provide enablement for (1) all isolated I-FLICE-2 polypeptide having an amino acid sequence "at least 95% identical" to amino acid sequence selected from the group consisting of: (a) amino acids from "about 1 to about 75 in SEQ ID NO: 6"; (b) amino acids from "about 76 to about 252 in SEQ ID NO: 6"; (c) amino acids from "about 253 to about 348 in SEO ID NO: 6"; (d) amino acids from "about 1 to about 348 in SEQ ID NO:6"; (e) amino acids from "about 2 to about 348 in SEQ ID NO:6"; and the amino acid sequence of an epitope-bearing portion of any one of the polypeptides mentioned above; (2) all isolated I-FLICE-2 polypeptide wherein the amino acid sequence "comprises" an antigenic region selected from the group consisting of: (i) amino acid residues from "about 62 to about 136 in SEQ ID NO: 6"; (ii) amino acids residues from "about 184 to about 193 in SEQ ID NO: 6" and (iii) amino acid residues from "about 205 to about 341 in SEQ ID NO: 6", and (3) all fusion protein comprising any isolated I-FLICE-2 polypeptide mentioned above fused to *any* "heterologous polypeptide". The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in **scope** with these claims.

Factors to be considered in determining whether undue experimentation is required to practice the claimed invention are summarized *In re Wands* (858 F2d 731, 737, 8

USPQ2d 1400, 1404 (Fed. Cir. 1988)). The factors most relevant to this rejection are the scope of the claim, the amount of direction or guidance provided, the lack of sufficient working examples, the unpredictability in the art and the amount of experimentation required to enable one of skill in the art to practice the claimed invention. The specification disclosure is insufficient to enable one skilled in the art to practice the invention as broadly claimed without an undue amount of experimentation.

The specification discloses only two I-FLICE polypeptides comprising SEQ ID NO: 2 (I-FLICE-1) and SEQ ID NO: 6 (I-FLICE-2) as shown in Figures 1 and 2 wherein the I-FLICE-2 polypeptide inhibits apoptosis mediated by TNFR-1 and CD95 (Figure 6).

The specification does not teach how to make *any* I-FLICE-2 polypeptide having at least "95% sequence identity" to amino acid sequence set forth in claims 9, 13, 15, 17 and 19 because there is insufficient guidance as to which amino acids within about 1 to about 75 in SEQ ID NO: 6, or within about 76 to about 252 in SEQ ID NO: 6 or within about 253 about 348 in SEQ ID NO: 6 to be substituted, deleted, added or any combination thereof and whether the resulting polypeptide maintains its anti-apoptotic activity. Further, the term "about" expands the specified amino acid residues of SEQ ID NO: 6 to include additional amino acids residues at either or both ends of the recited residues. Given the ambiguity of the specified amino acid residues, there is insufficient guidance as how to make at least 95% sequence identity to the said polypeptide. Likewise, there is insufficient guidance as to which amino acids within the full length sequence from about 1 to about 348 or about 2 to about 348 SEQ ID NO: 6 to be substituted, deleted or added and whether the resulting polypeptide maintains anti-apoptotic activity. A polypeptide with at least 95% identity means at least 5% differences which is equivalent to having at least 18 amino acids modification such as substitution, deletion, addition and combination thereof. There is a lack of working example demonstrating all undisclosed I-FLICE-2 polypeptide mentioned above are effective for inhibiting apoptosis, much less for treating any apoptosis related diseases.

It is known in the art that the relationship between the amino acid sequence of a protein (polypeptide) and its tertiary structure (i.e. its binding activity) are not well understood and are not predictable (see Ngo et al., in The Protein Folding Problem and Tertiary Structure Prediction, 1994, Merz, et al., (ed.), Birkhauser, Boston, MA, pp. 433 and 492-495).

There is no recognition in the art that sequence with identity predicts biological function. It is known in the art that even a single amino acid changes or differences in a protein's amino acid sequence can have dramatic effects on the protein's function. Mikayama *et al.*, teach that the

human glycosylation-inhibiting factor (GIF) protein differs from human macrophage migration inhibitory factor (MIF) by a single amino acid residue (Figure 1 in particular). Yet, Mikayama *et al.* further teach that GIF is unable to carry out the function of MIF and MIF does not demonstrate GIF bioactivity (Abstract in particular). It is also known in the art that amino acid sequence determines the function of the polypeptide or protein. However, the predictability of which changes can be tolerated in an amino acid sequence and still retain similar functions and properties requires a knowledge of, and guidance such as which amino acids within the full-length polypeptide are tolerant of modification and which amino acid residues are conserved or less tolerant to modification in which the product's structure relates to its functional usefulness.

The use of "percent" in conjunction with any of the various terms that refer to sequence identity or similarity is a problem because sequence identity between two sequences has no common meaning within the art. The term "percent" is relative and can be defined by the algorithm and parameter values set when using the algorithm used to compare the sequences. The scoring of gaps when comparing one sequence to another introduces uncertainty as to the percent of similarity between two sequences. Because applicants have not disclosed the specific condition used to score sequence identity while using any computer program mentioned above, it is unpredictable to determine which amino acid sequences will have at least about 95% identity to the claimed sequence and still retains the activities. In addition to the problem of having "at least 95% identity" mentioned above, the term "about" compounds the problem by extending the lower and upper limits of the amino acids residues in SEQ ID NO: 6 or the full length polypeptide of SEQ ID NO: 6. Further, the term "having" or "comprises" is open-ended. It expands the polypeptide fragment such as the ones recited in claim 21 to include additional amino acids at either or both ends. There is insufficient guidance as to which amino acids to be added and whether the undisclosed has any function, let alone a method of treating any disease using the claimed polypeptide.

Attwood *et al.* teach that protein function is context-dependent and the state of the art of making functional assignments merely on the basis of some degree of similarity between sequences and the current structure prediction methods is unreliable (See figure, entire document).

Skolnick *et al* teach that sequence-based methods for function prediction are inadequate and knowing a protein's structure does not tell one its function (See abstract, in particular).

It is unpredictable which undisclosed polypeptide having at least about 95 amino acid differences would maintain its structure and biological function such as inhibiting apoptosis by TNFR-1 and/or CD95, in turn, would be useful for treating all diseases associated with apoptosis such as the ones listed on page 27. Further, there is no in vivo working example demonstrating that any isolated polypeptide mentioned above including the full length I-FLICE-2 comprising SEQ ID NO: 6 could treat all diseases associated with apoptosis. Until the activity associated with the polypeptide having at least 95% sequence identity to the polypeptides mentioned above has been identified, the specification merely extends an invitation to one skill in the art for further experimentation to arrive at the claimed invention.

For these reasons, it would require undue experimentation of one skilled in the art to practice the claimed invention. See page 1338, footnote 7 of Ex parte Aggarwal, 23 USPQ2d 1334 (PTO Bd. Pat App. & Inter. 1992).

In re wands, 858 F.2d at 737, 8 USPQ2d at 1404 (Fed. Cir. 1988), the decision of the court indicates that the more unpredictable the area is, the more specific enablement is necessary. In view of the quantity of experimentation necessary, the limited working examples, the unpredictability of the art, the lack of sufficient guidance in the specification and the breadth of the claims, it would take an undue amount of experimentation for one skilled in the art to practice the claimed invention.

Applicants' arguments filed 12/20/04 have been fully considered but are not found persuasive.

Applicants' position is that to satisfy the enablement requirement, the specification must enable a person of ordinary skill in the art to practice a single use of the claimed polypeptides without undue experimentation. See, e.g., MPEP j2164.01(c). The Examiner has not provided sufficient evidence or a basis to question the enablement provided in the specification for the claimed polypeptides. All of these references Ngo, Attwood, Skolnick and discuss the limitations of using computational analyses in assigning function to genomic sequences based on similarity found through searching known databases of genes. They do not address nor question the predictability of making a variant with a particular percent identity and testing it for a known activity. The Examiner has further cited Mikayama et al. in support of the proposition that "even single amino acids changes ... can have dramatic effects on the protein's function." See, section 9, page 7, First paragraph. Applicants respectfully disagree with the Examiner's contention. While this proposition may be true for very specific amino acid changes in the particular protein -

human GIF - which is the subject of the reference, Applicants note that Mikaynma et al. does not discuss whether changes at any other of the 114 positions alter the biological activity of GIF. Thus, the observations of Mikaynma et al. relating to a particular GIF amino acid position do not necessarily extend to all other amino acid positions in GIF, much less to positions in other proteins such as I-FLICE-Z. Therefore, the cited reference fails to support the assertion that any and all amino acid changes in I-FLICE-Z would have a dramatic effect on activity. Even assuming arguendo that the situation reported in Mikayama is representative of all amino acid positions in GIF', it is not representative of all proteins or all amino acid substitutions, deletions, and insertions. Numerous publications in the art support the contention that, in general, proteins are resilient to modification and retain functional activity notwithstanding numerous amino acid substitutions, deletions, and insertions. For example, the specification discloses that Bowie, J.U. et al., "Deciphering the Message in Protein Sequencing: Tolerance to Amino Acid Substitutions" Science 247:1306-1310 (1990) provides guidance concerning how to make phenotypically silent amino acid substitutions. See, specification, for example, at page 15-16, paragraph 48; and at page 18, paragraph 59. A further example of the tolerance of proteins to amino acid modification is provided by Gayle et a1., "Identification of regions in Interleukin-la important for activity" J. Biol. Chem. 26842%:22105-2211141993) (submitted herein as Exhibit B). This reference discloses the use of random mutagenesis to generate over 3,500 individual IL-la mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible amino acid position. The investigators found that "most of the molecule could be altered with little effect on either binding or biological activity." In fact, only 23 unique amino acid sequences, out of more 111a1,1 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type. There are ample guidance provided in the specification on how to make, test and use the claimed polypeptides to inhibit TNFR-1 and CD95-induced apoptosis. See, specification, for example, at page 3, paragraph 5; at page 4, paragraph 9; at page 7-8, paragraph 23; and at page 18, paragraph 59. 'The specification further teaches how to make, screen, and use the claimed polypeptides. In addition to the amino acid sequence common to the polypeptides of the claimed invention (e.g., SEQ ID NO:6), the specification further provides sample disclosure of other relevant characteristics of the claimed polypeptides. First, the specification provides the parameters used to determine the percent identity of the polypeptides of the claimed invention. See, for example, specification at page 21, paragraph 67 to page 22, paragraph 71. The specification further

provides a detailed analysis of the structural attributes of the I-FLICE-2 protein, including important domains of the protein. See, for example, specification at page 7, paragraph 23. Moreover, the specification provides guidance on how to make variants which fall within the scope of the instant invention by insertion, deletion, inversions, repeats, and type substitutions. See, specification, for example, at page 18, paragraph 59 to page 22, paragraph 71. The specification also provides a detailed analysis of the functional attributes of the I-FLICE-Z protein, such as, for example, antigenic index of the I-FLICE-2 polypeptide. See, specification, for example, at page 5, paragraph 17; and at Figure 5. Thus, the specification provides ample direction to the skilled artisan as to which amino acids of SEQ ID NO:6 are suitable to modify without substantially affecting activity. Additionally, the specification also teaches the skilled artisan how to screen these variants for the ability to inhibit TNFR-I and CD-95 induced apoptosis. In particular, the specification teaches a cell death assay useful for measuring the apoptotic activity of 1-FLICE-2 polypeptides. See, specification, for example, at page 5, paragraph 18; at page 15, paragraph 46, at Example 6, page 54, paragraph 192 to page 55, paragraph 194.

In response, amended claim 9 still recites an isolated I-FLICE-2 polypeptide having an amino acid sequence at least "95% identical" to a sequence selected from the group consisting of:

(a) amino acids from 1 to 75 in SEQ m NO: 6;

(b) amino acids from 76 to 252 in SEQ ID N0: 6;

(c) amino acids from 253 to 348 in SEQ ID N0:6;

(d) amino acids from 1 to 348 in SEQ ID N0:6;

(e) amino acids from 2 to 348 in SEQ ID N0:6;

(f) the amino acid sequence of the I-FLICE-2 polypeptide having the amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 209038, and

(g) the amino acid sequence of an "epitope-bearing portion" of any one of the polypeptides of (a), (b), (c), (d), (e), or (f), wherein said I-FLICE-Z polypeptide inhibits TNFR-I and CD-95 induced apoptosis.

The specification does not teach how to make *any* I-FLICE-2 polypeptide having at least "95% sequence identity" to amino acid sequence set forth in claims 9, 13, 15, 17 and 19 because there is insufficient guidance as to which amino acids within 1 to about 75 in SEQ ID NO: 6, 76 to about 252 in SEQ ID NO: 6, 253 to 348 in SEQ ID N0: 6, or amino acid sequence of the I-

FLICE-2 polypeptide encoded by the cDNA clone contained in ATCC Deposit No 209038 or which "epitope-bearing portion" of any one of said polypeptide to be substituted, deleted, added or any combination thereof and whether the resulting polypeptide maintains its anti-apoptotic activity. There is a insufficient working example demonstrating any undisclosed I-FILICE-2 having merely 95% sequence identity to any of the sequence mentioned above has anti-apoptotic activity, much less for treating any and all diseases or disorders using the claimed polypeptide. Further, the term "having" in claim 9 or "comprises" in claim 21 is open-ended. It expands the fragment of claim 9 (a), (b), (c) and (g) to include additional amino acids at either of both ends. There is a lack of guidance as to which amino acids to be added and whether the resulting polypeptide inhibits TNFR-1 and CD-95 induced apoptosis.

As evidence by the teachings of Ngo et al, the relationship between the amino acid sequence of a protein (polypeptide) and its tertiary structure (i.e. its binding activity) are not well understood and are not predictable (see Ngo et al., in The Protein Folding Problem and Tertiary Structure Prediction, 1994, Merz, et al., (ed.), Birkhauser, Boston, MA, pp. 433 and 492-495). Without the amino acid sequence of any polypeptide as set forth in claim 9, one skill in the art cannot make, much less use the claimed invention. Attwood *et al.* teach that protein function is context-dependent and the state of the art of making functional assignments merely on the basis of some degree of similarity between sequences and the current structure prediction methods is unreliable (See figure, entire document). Skolnick *et al* teach that sequence-based methods for function prediction are inadequate and knowing a protein's structure does not tell one its function (See abstract, in particular). There is no recognition in the art that sequence with identity predicts biological function. Mikayama *et al.* teach that even a single amino acid changes or differences in a protein's amino acid sequence can have dramatic effects on the protein's function. Until the amino acids within the sequences as set forth in claims 9, 13, 15, 17, and 19 that are tolerance of change have been determined and the polypeptide having at least 95% sequence identity to the polypeptides mentioned above associated with which particular activity has been identified, the specification as filed merely extends an invitation to one skill in the art for further experimentation to arrive at the claimed invention.

In response to applicant's cited references in Exhibit B, none of the references are provided. There is no Exhibit B in the amendment filed 12/20/04.

6. No claim is allowed.

7. **THIS ACTION IS MADE FINAL.** See MPEP § 706.07(a).

Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a). A shortened statutory period for response to this final action is set to expire THREE MONTHS from the date of this action. In the event a first response is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event will the statutory period for response expire later than SIX MONTHS from the date of this final action.

8. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Phuong Huynh "NEON" whose telephone number is (571) 272-0846. The examiner can normally be reached Monday through Friday from 9:00 am to 5:30 p.m. A message may be left on the examiner's voice mail service. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Christina Chan can be reached on (571) 272-0841. The IFW official Fax number is (571) 273-8300.

9. Any information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

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